REMARKS

By a Notice dated February 25, 2002 in the file of this application, the Patent and Trademark Office informed the applicants, through the undersigned, about parts missing in connection with the filing of this application. The missing parts were the Declaration and Power of Attorney executed by the inventors of this application.

Enclosed herewith are duplicate Declarations and Powers of Attorney which, in the aggregate, are executed by all three of the inventors of this patent application.

Separately included with this submission is a Sequence Listing suitable for this patent application in both paper and computer readable form. The content of the paper and computer readable copies of the sequence listing submitted herewith are the same. No new matter is introduced by the submission and the accompanying amendments.

Per 37 C.F.R. §1.121(d), the applicants submit the enclosed Fig. 2 for replacing the Fig. 2 in the application with the proposed changes marked in red. Approval of the changes is respectfully requested. Upon Examiner's approval, new Fig. 2 including the changes will be filed.

It is believed that these submissions complete the formalities acquired in connection with the filing of this patent application. Examination on the merits is respectfully requested.

An extension of time is submitted herewith so that this Response will be considered as timely filed.

Respectfully submitted,

Zhibin Ren
Reg. No.: 47,897
Attorney for Applicants
QUARLES & BRADY LLP
P.O. Box 2113
Madison, WI 53701

TEL 608/251-5000
FAX 608/251-9166

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Applicants: Cynthia A. Henson
Elizabeth H. Muslin
Suzanne E. Clark

Date: June 19, 2002

Serial No.: 10/043,418

Group Art Unit:

Filed: 01/10/2002

Examiner:

Title: MODIFIED BARLEY ALPHA-GLUCOSIDASE

File No.: 960296.97486

In the specification:

Please replace paragraph 00015 spanning from page 3 to page 4 of the application with the following:

--[00015] To facilitate this process, an alignment study of the various known plant α-glucosidase genes was conducted. This alignment is represented in an alignment table, shown in Fig. 2. Fig. 2 shows the best-fit alignment of the amino acid sequence of the α-glucosidase genes from barley, sugar beet, spinach and Arabidopsis (provided as SEQ ID NO:1, 2, 3 and 4, respectively), using the conventional single letter representations for the amino acids. Capital letters indicate identity to the barley sequence. This sequence comparison information can be combined with information about predicted secondary structure of the protein, available from computer analysis of the sequence, to begin to identify sites for mutation to create better thermostability.--

Please replace paragraph 00031 on page 9 of the application with the following:

--[00031] Mutagenesis. Mutagenesis was done using the Muta-Gene kit (BIO-RAD). Barley α-glucosidase cDNA was sub-cloned into the EcoRI site of the phagemid pTZ18U (BIO-RAD, Hercules, CA). E. coli strain CJ236 (Kunkel et al., 1987) was used to generate dU-substituted DNA and single stranded DNA was isolated using the helper phage M13K07 (BIO-RAD). For the mutant R336P, the oligonucleotide CGGTGAAGTTGACAGGATCCAAGGTGAAG (SEQ ID NO:5) (5', reverse complement) was used to replace the codon for arginine (CGT) with a codon for proline (CCT) and to remove a Tth111I site. For the mutant T340P, the oligonucleotide GAGCTCGGCGGCGGGGAAGTTTACACGGTC (SEQ ID NO:6) was used to replace the codon for threonine (ACC) with a codon for proline (CCC) and to remove a Tth111I site. For the mutant A742P, the

oligonucleotide CCAGGAGGTGGAACGGGGTCCGGCGC (SEQ ID NO:7) was used to replace the codon for alanine (GCG) with a codon for proline (CCG) and to remove a RsrII site.--